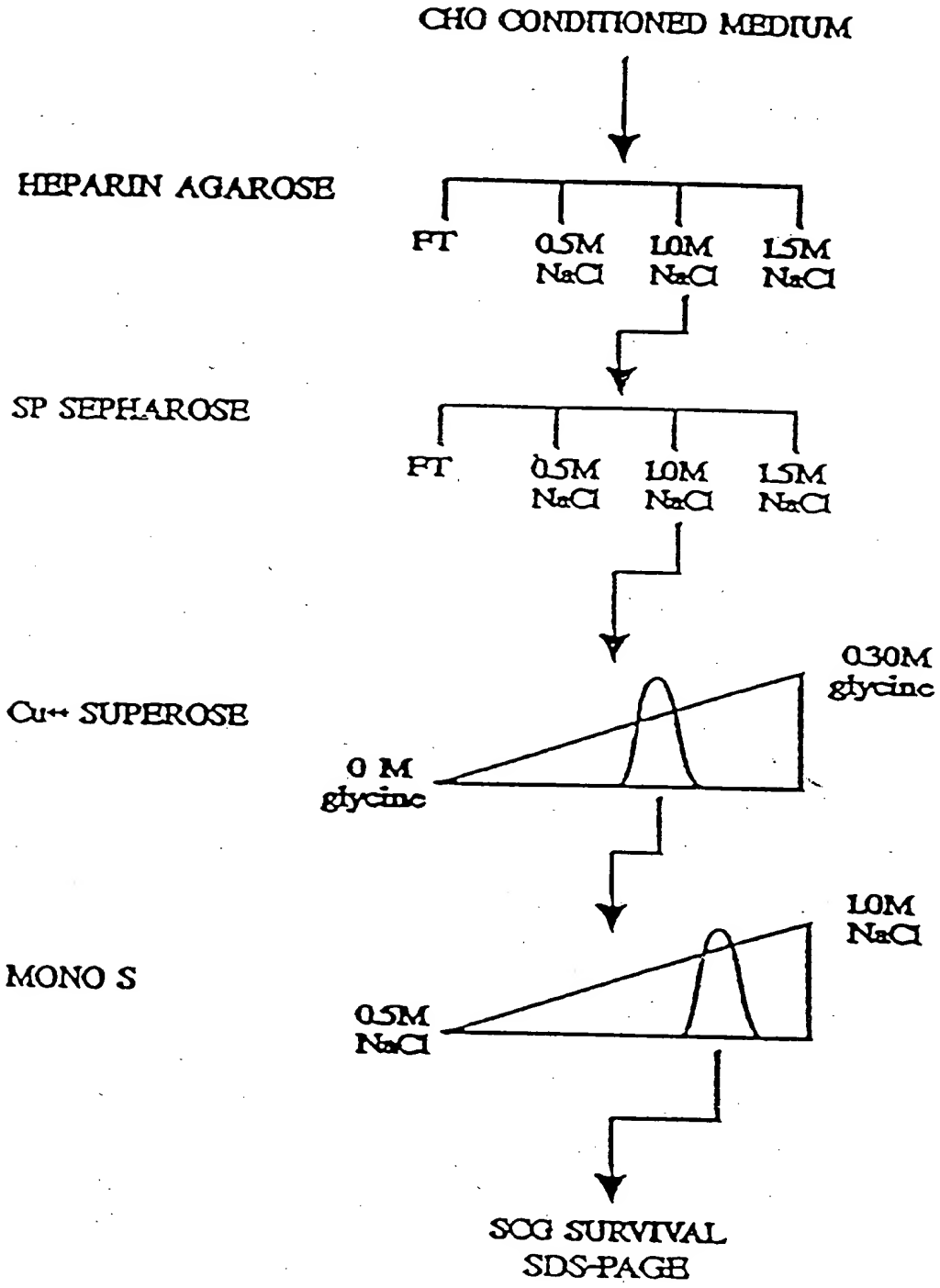
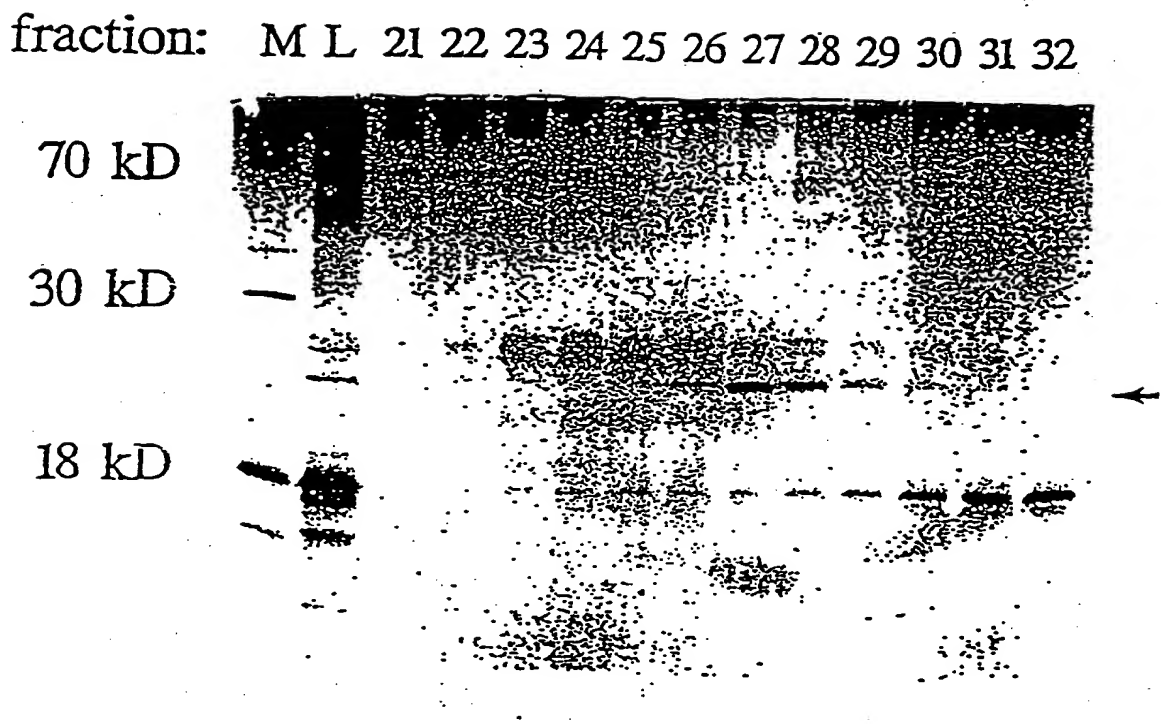

CHO CONDITIONED MEDIUM
HEPARIN AGAROSE
FT
0.5M NaCl
1.0M NaCl
1.5M NaCl
SP SEPHAROSE
FT
0.5M NaCl
1.0M NaCl
1.5M NaCl
Cu++ SUPEROSE
0.30M glycine
0 M glycine
MONO S
1.0M NaCl
0.5M NaCl
SOG SURVIVAL
SDS-PAGE

Figure 1


fraction: M L 21 22 23 24 25 26 27 28 29 30 31 32
70 kD
30 kD
18 kD

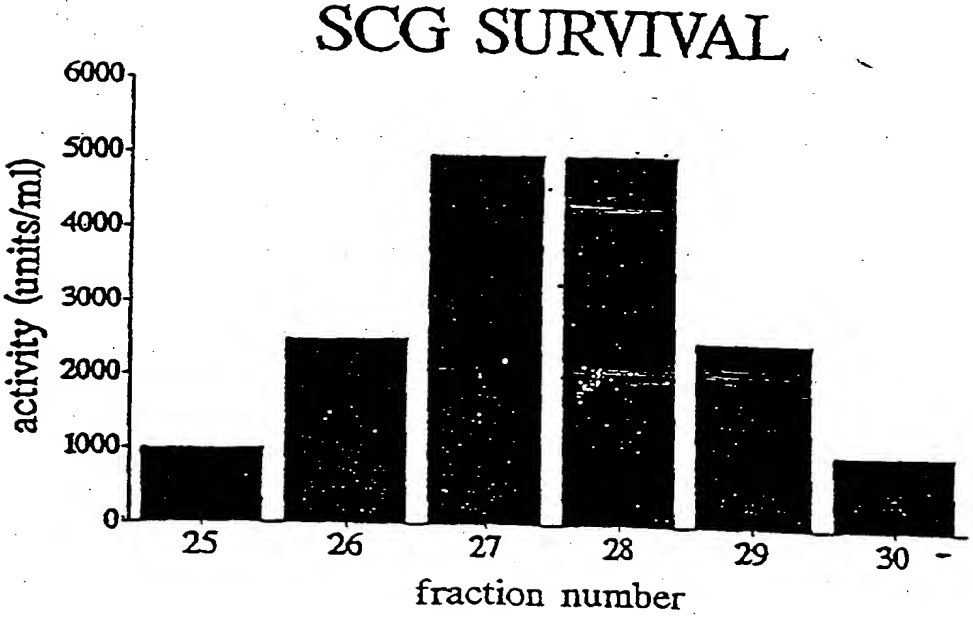
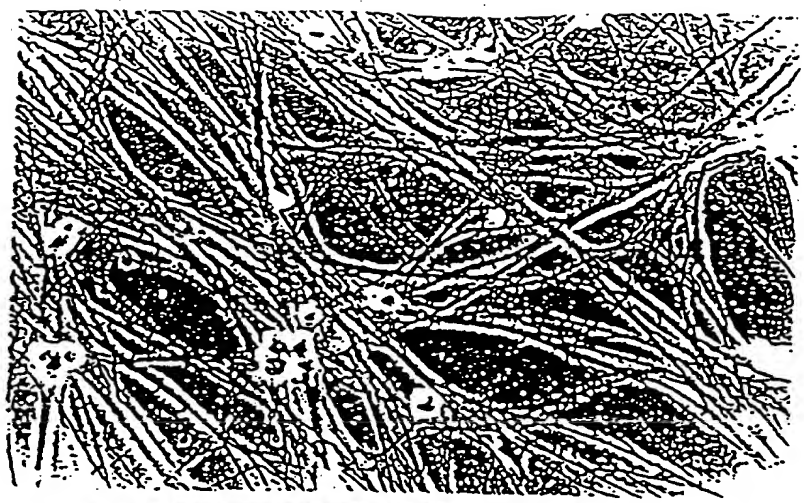
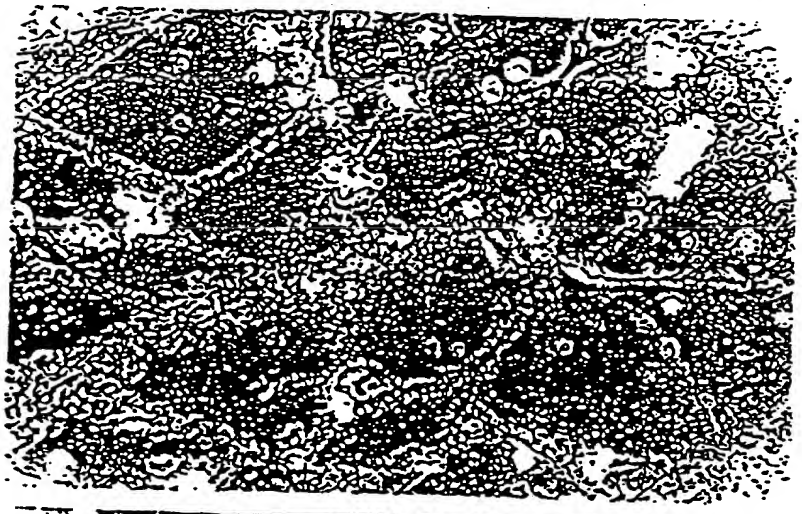

SCG SURVIVAL
activity (units/ml)
6000
5000
4000
3000
2000
1000
0
25
26
27
28
29
30
fraction number

Figure 2

A) NGF



B) Anti-NGF



C) Anti-NGF
+
Neurturin

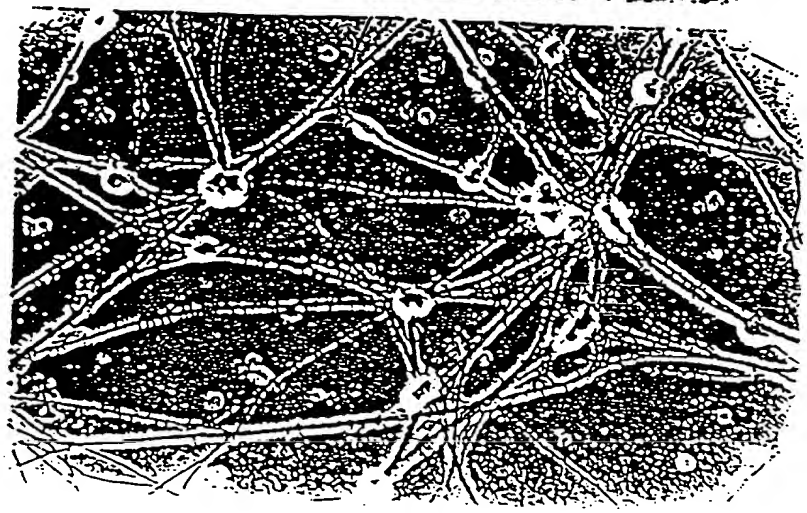


Figure 3

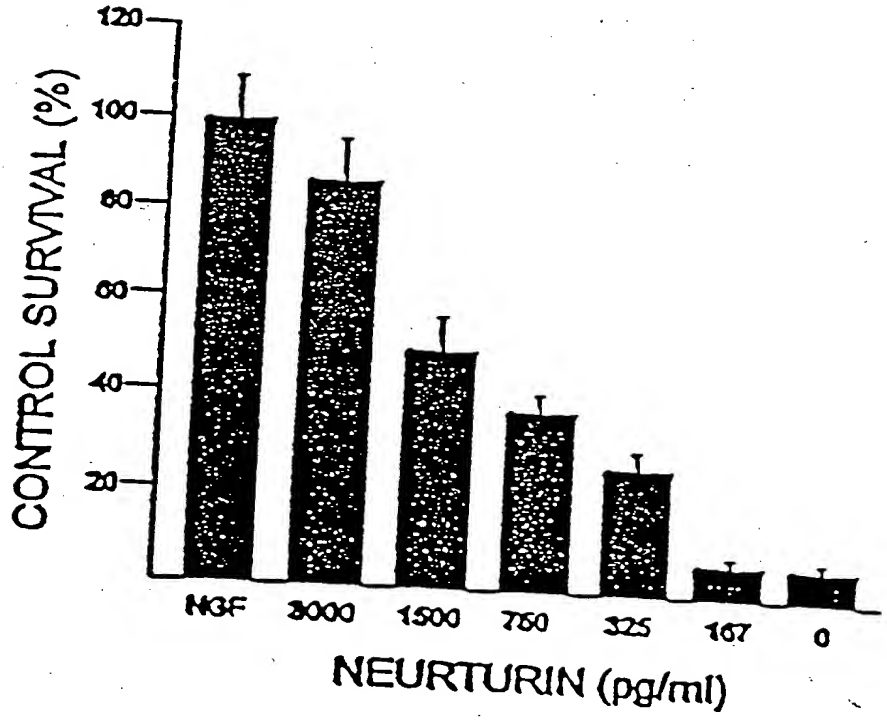

CONTROL SURVIVAL (%)
120
100
80
60
40
20
NGF
3000
1500
750
325
167
0
NEURTURIN (pg/ml)

Figure 4

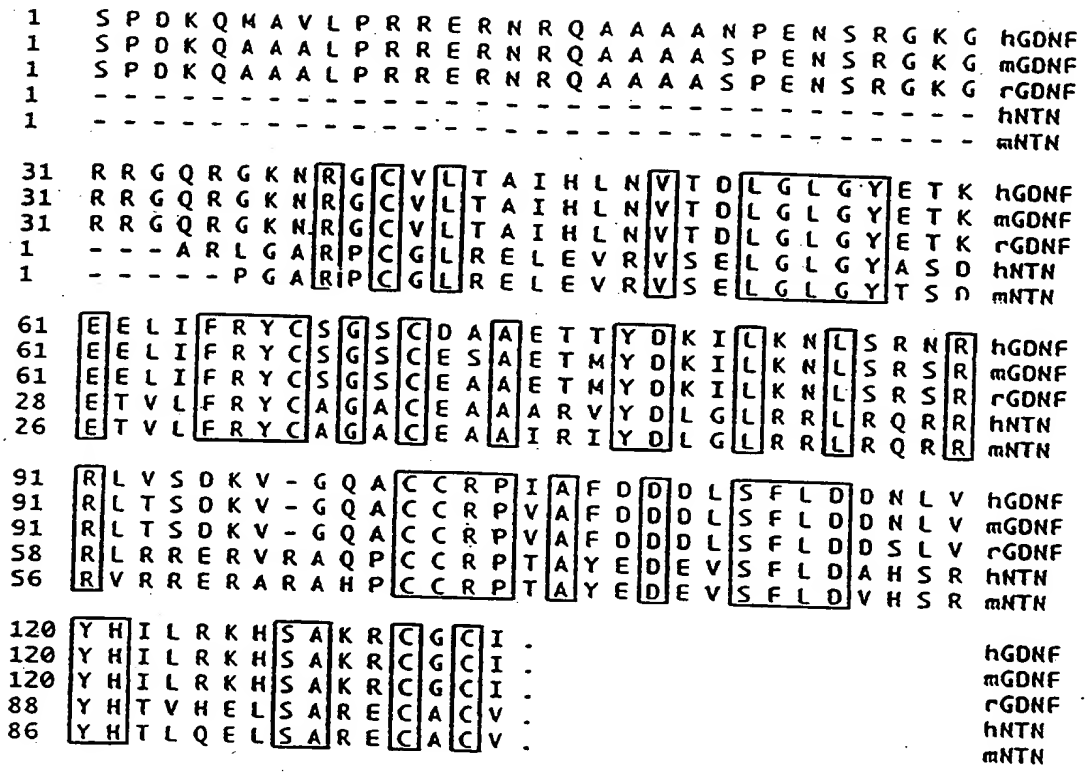

1 S P D K Q M A V L P R R E R N R Q A A A A N P E N S R G K G hGDNF
1 S P D K Q A A A L P R R E R N R Q A A A A S P E N S R G K G mGDNF
1 S P D K Q A A A L P R R E R N R Q A A A A S P E N S R G K G rGDNF
1 - hNTN
1 - mNTN
31 R R G Q R G K N R G C V L T A I H L N V T D L G L G Y E T K hGDNF
31 R R G Q R G K N R G C V L T A I H L N V T D L G L G Y E T K mGDNF
31 R R G Q R G K N R G C V L T A I H L N V T D L G L G Y E T K rGDNF
1 - - - A R L G A R P C G L R E L E V R V S E L G L G Y A S D hNTN
1 - - - - - - P G A R P C G L R E L E V R V S E L G L G Y T S D mNTN
61 E E L I F R Y C S G S C D A A E T T Y D K I L K N L S R N R hGDNF
61 E E L I F R Y C S G S C E S A E T M Y D K I L K N L S R S R mGDNF
61 E E L I F R Y C S G S C E A A E T M Y D K I L K N L S R S R rGDNF
28 E T V L F R Y C A G A C E A A A R V Y D L G L R R L R Q R R hNTN
26 E T V L F R Y C A G A C E A A I R I Y D L G L R R L R Q R R mNTN
91 R L V S D K V - G Q A C C R P I A F D D D L S F L D D N L V hGDNF
91 R L T S D K V - G Q A C C R P V A F D D D L S F L D D N L V mGDNF
91 R L T S D K V - G Q A C C R P V A F D D D L S F L D D S L V rGDNF
58 R L R R E R V R A Q P C C R P T A Y E D E V S F L D A H S R hNTN
56 R V R R E R A R A H P C C R P T A Y E D E V S F L D V H S R mNTN
120 Y H I L R K H S A K R C G C I . hGDNF
120 Y H I L R K H S A K R C G C I . mGDNF
120 Y H I L R K H S A K R C G C I . rGDNF
88 Y H T V H E L S A R E C A C V . hNTN
86 Y H T L Q E L S A R E C A C V . mNTN

Figure 5

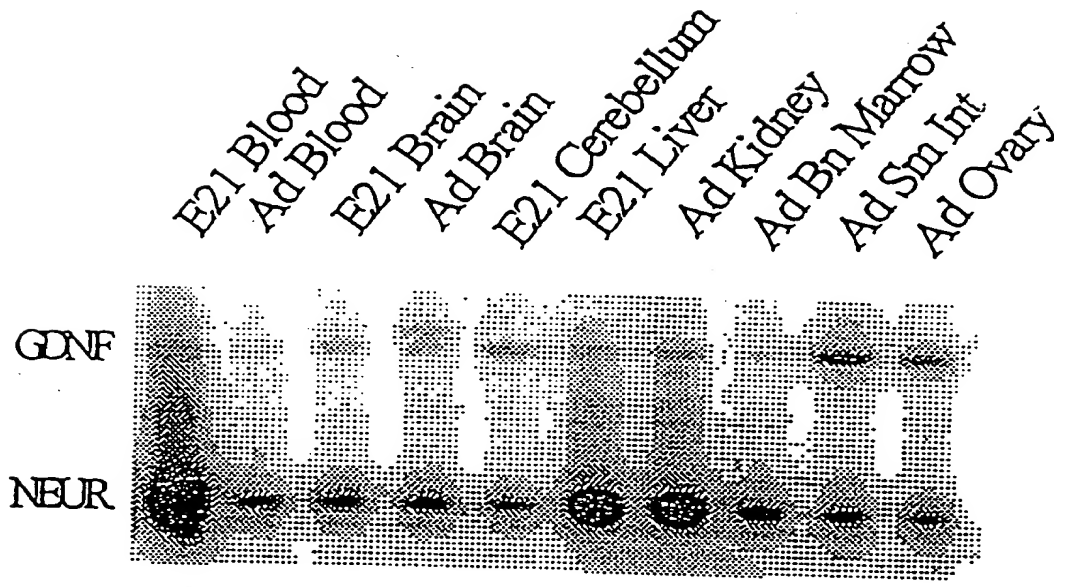

E21 Blood
Ad Blood
E21 Brain
Ad Brain
E21 Cerebellum
E21 Liver
Ad Kidney
Ad Bn Marrow
Ad Sm Int
Ad Ovary
GDNF
NEUR

Figure 6

```
ATGCAGCGCTGGAAGGCGGCGGCCTTGGCCTCAGTGCTCTGCAGCTCCGTGCTGTCCATC 60
Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser Val Leu Ser Ile

TGGATGTGTCGAGAGGGCCTGCTTCTCAGCCACCGCCTCGGACCTGCGCTGGTCCCCCTG 120
Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro Ala Leu Val Pro Leu

CACCGCCTGCCTCGAACCCTGGACGCCCGGATTGCCCGCCTGGCCCAGTACCGTGCACTC 180
His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu

CTGCAGGGGGCCCCGGATGCGATGGAGCTGCGCGAGCTGACGCCCTGGGCTGGGCGGCCC 240
Leu Gln Gly Ala Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro

CCAGGTCCGCGCCGTCGGGCGGGGCCCCGGCGGCGGCGCGCGCGTGCGCGGTTGGGGGCG 300
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala Arg Leu Gly Ala

CGGCCTTGCGGGCTGCGCGAGCTGGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTACGCG 360
Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala

TCCGACGAGACGGTGCTGTTCCGCTACTGCGCAGGCGCCTGCGAGGCTGCCGCGCGCGTC 420
Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val

TACGACCTCGGGCTGCGACGACTGCGCCAGCGGCGGCGCCTGCGGCGGGAGCGGGTGCGC 480
Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg

GCGCAGCCCTGCTGCCGCCCGACGGCCTACGAGGACGAGGTGTCCTTCCTGGACGCGCAC 540
Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His

AGCCGCTACCACACGGTGCACGAGCTGTCGGCGCGCGAGTGCGCCTGCGTGTGA 594
Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
```

Figure 7

```
ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTCGCTCATCTGCAGCTCCCTGCTATCTGTC  60
Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser Leu Leu Ser Val

TGGATGTGCCAGGAGGGTCTGCTCTTGGGCCACCGCCTGGGACCCGCGCTTGCCCCGCTA  120
Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro Ala Leu Ala Pro Leu

CGACGCCCTCCACGCACCCTGGACGCCCGCATCGCCCGCCTGGCCCAGTATCGCGCTCTG  180
Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu

CTCCAGGGCGCCCCCGACGCGGTGGAGCTTCGAGAACTTTCTCCCTGGGCTGCCCGCATC  240
Leu Gln Gly Ala Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile

CCGGGACCGCGCCGTCGAGCGGGTCCCCGGCGTCGGCGGGCGCGGCCGGGGGCTCGGCCT  300
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro Gly Ala Arg Pro

TGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTACACGTCGGAT  360
Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Thr Ser Asp

GAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCGAGGCGGCCATCCGCATCTACGAC  420
Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp

CTGGGCCTTCGGCGCCTGCGCCAGCGGAGGCGCGTGCGCAGAGAGCGGGCGCGGGCGCAC  480
Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His

CCGTGTTGTCGCCCGACGGCCTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGC  540
Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg

TACCACACGCTGCAAGAGCTGTCGGCGCGGGAGTGCGCGTGCGTGTGA  588
Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val *
```

Figure 8

GGAGGGAGAGCGCGCGGTGGTTTCGTCCGTGTGCCCCGCGCCCGGCGC -301

TCCTCGCGTGGCCCCGCGTCCTGAGCGCGCTCCAGCCTCCCACGCGCGCC -251

ACCCCGGGGTTCACTGAGCCCGGCGAGCCCGGGGAAGACAGAGAAAGAGA -201

GGCCAGGGGGGGAACCCCATGGCCCGGCCCGTGTCCCGCACCCTGTGCGG -151

TGGCCTCCTCCGGCACGGGGTCCCCGGGTCGCCTCCGGTCCCCGCGATCC -101

GGATGGCGCACGCAGTGGCTGGGGCCGGGCCGGGCTCGGGTGGTCGGAGG -51

AGTCACCACTGACCGGGTCATCTGGAGCCCGTGGCAGGCCGAGGCCCAGG -1

ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTCGCTCATCTGCAGCTCCCT 50

GCTATCTGTCTGGATGTGCCAGGAGGGTCTGCTCTTGGGCCACCGCCTGG 100

GACCCGCGCTTGCCCCGCTACGACGCCCTCCACGCACCCTGGACGCCCGC 150

ATCGCCCGCCTGGCCCAGTATCGCGCTCTGCTCCAGGGCGCCCCCGACGC 200

GGTGGAGCTTCGAGAACTTTCTCCCTGGGCTGCCCGCATCCCGGGACCGC 250

GCCGTCGAGCGGGTCCCCGGCGTCGGCGGGCGCGGCCGGGGGCTCGGCCT 300

TGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTA 350

CACGTCGGATGAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCGAGG 400

CGGCCATCCGCATCTACGACCTGGGCCTTCGGCGCCTGCGCCAGCGGAGG 450

CGCGTGCGCAGAGAGCGGGCGCGGGCGCACCCGTGTTGTCGCCCGACGGC 500

CTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGCTACCACACGC 550

TGCAAGAGCTGTCGGCGCGGGAGTGCGCGTGCGTGTGATGCTACCTCACG 600

CCCCCCGACCTGCGAAAGGGCCCTCCCTGCCGACCCTCGCTGAGAACTGA 650

CTTCACATAAAGTGTGGGAACTCCC 675

Figure 9

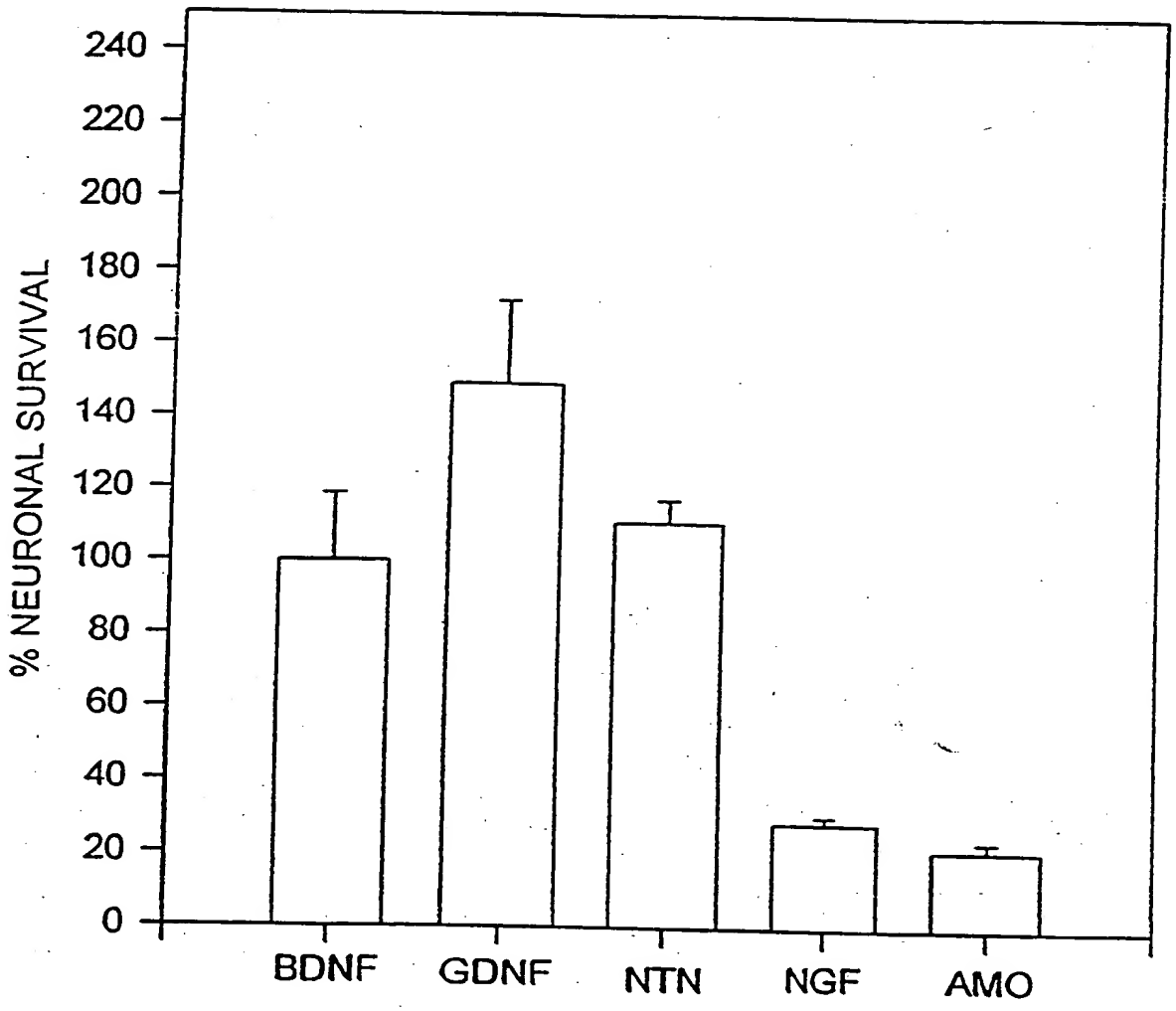

% NEURONAL SURVIVAL
240
220
200
180
160
140
120
100
80
60
40
20
0
BDNF
GDNF
NTN
NGF
AMO

Figure 10

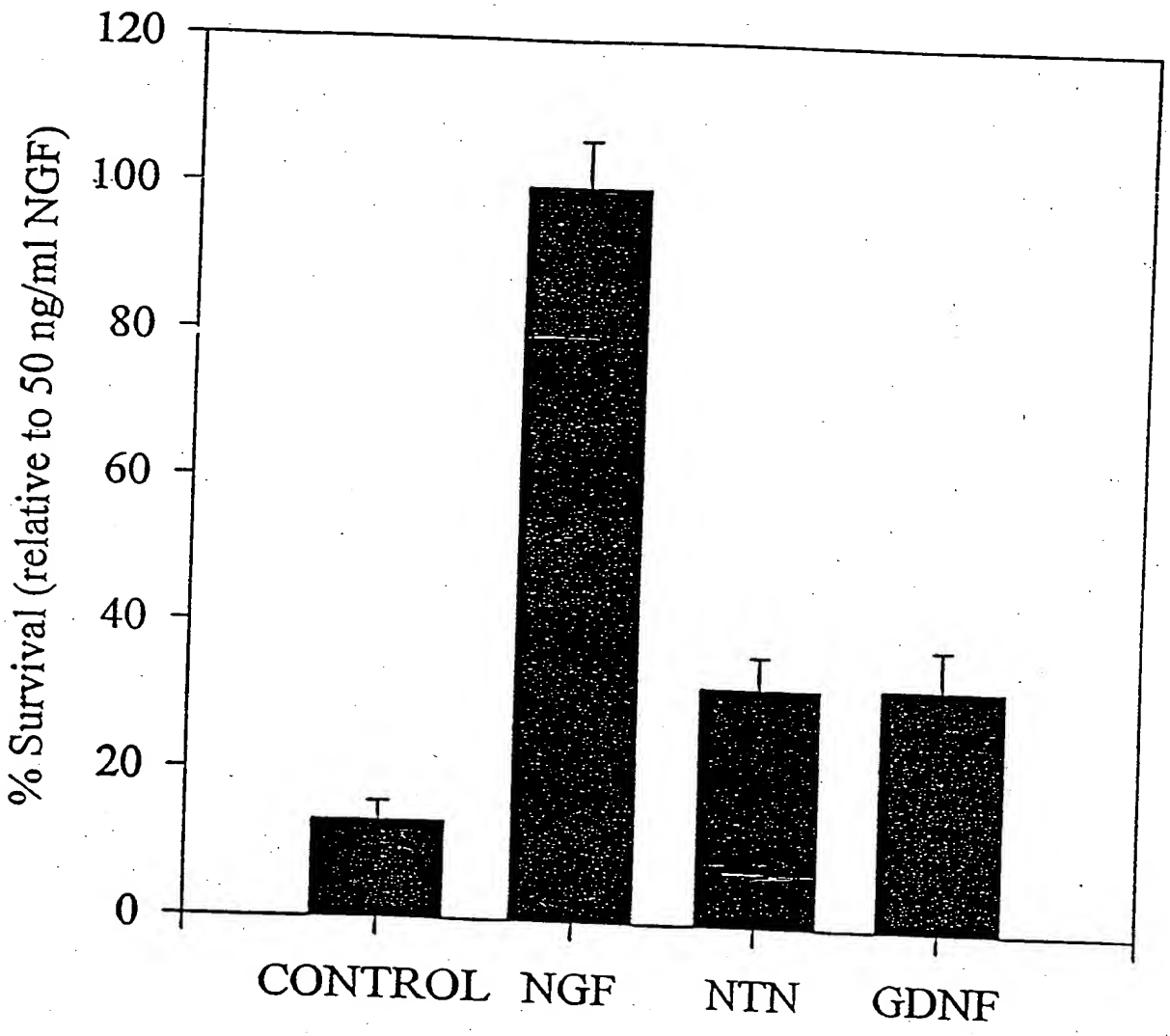

120
100
80
60
40
20
0
% Survival (relative to 50 ng/ml NGF)
CONTROL
NGF
NTN
GDNF

FIGURE 11

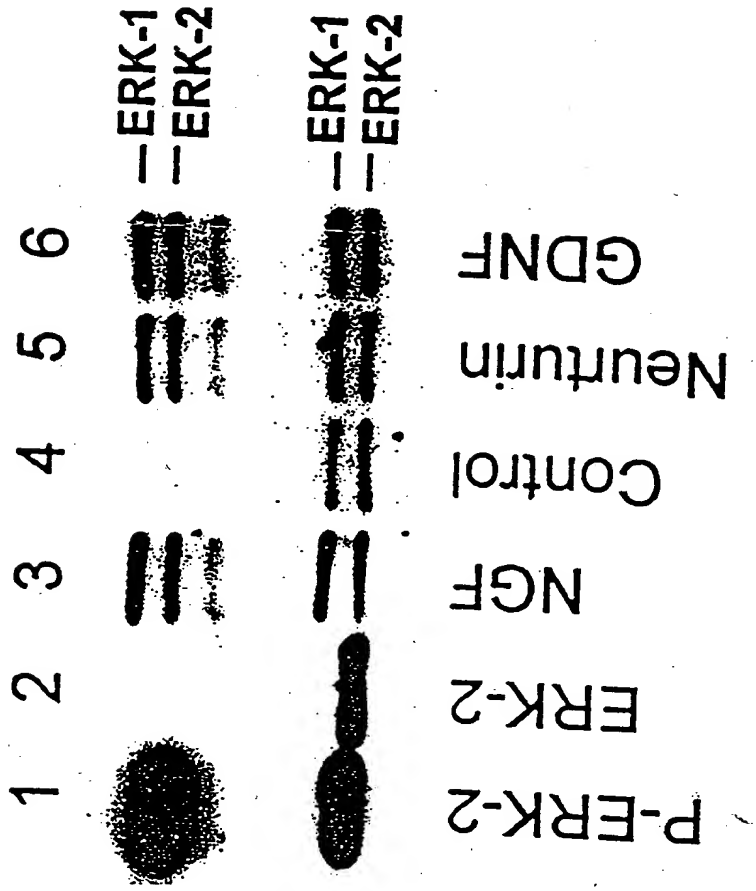


FIGURE 12A

FIGURE 12B

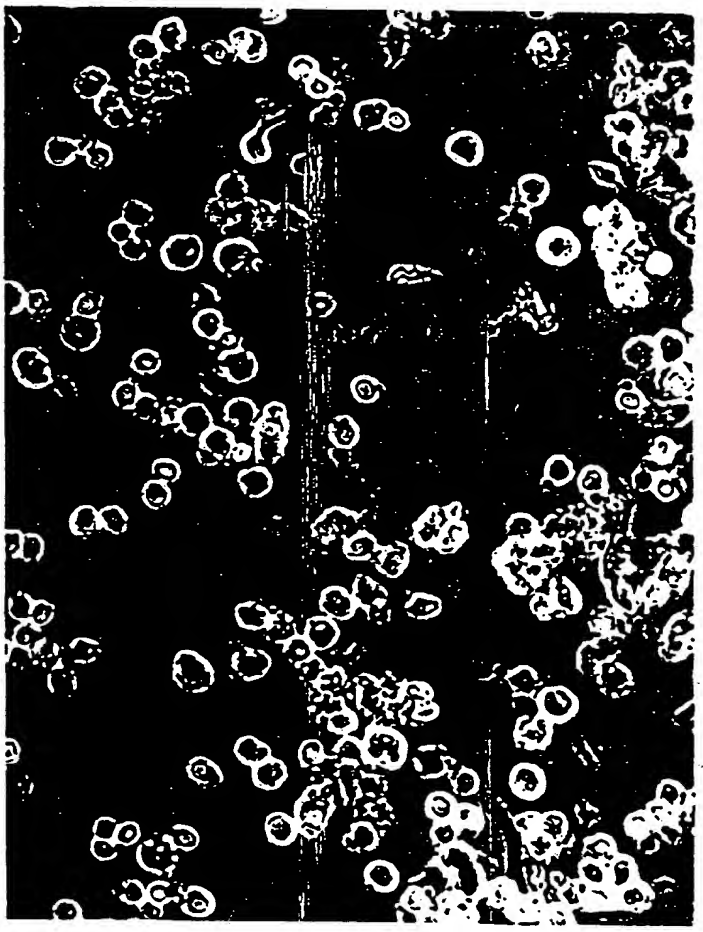


FIGURE 13 A. Untreated

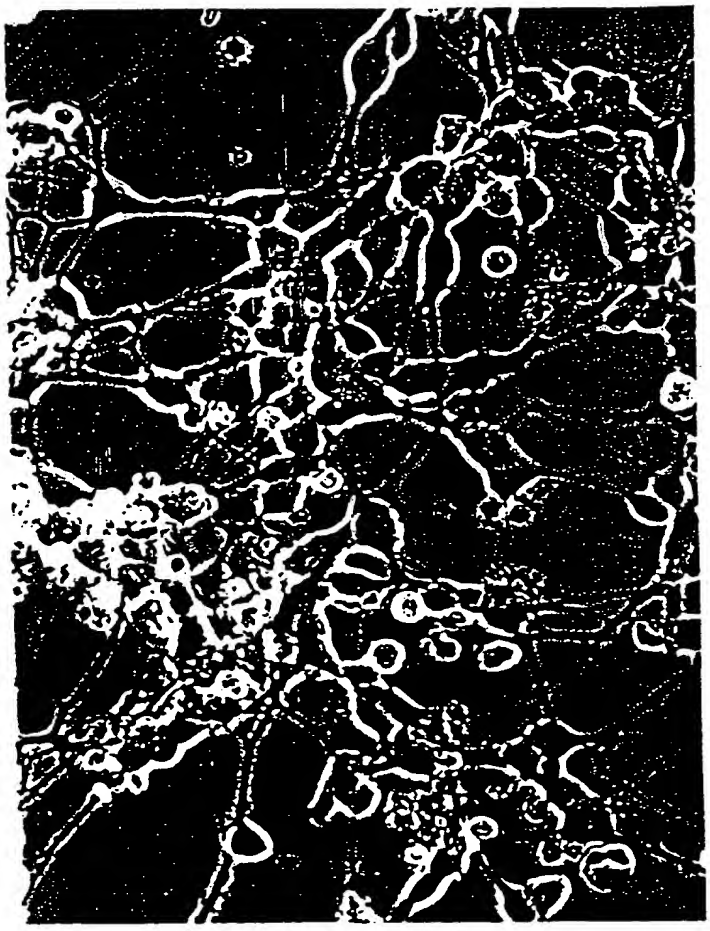


FIGURE 13 B. Neurturin-treated

MAPK Response in Neuroblastoma Cell Lines

SK-NSH Neuroblastoma (naive)

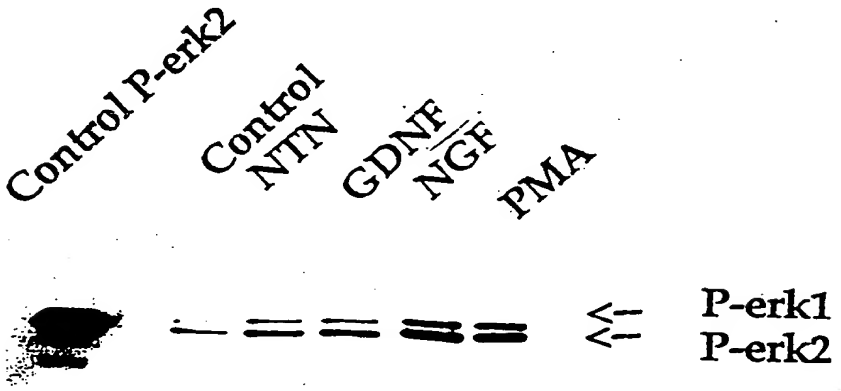


FIGURE 14A

FIGURE 14B NGP Neuroblastoma (RA tx)

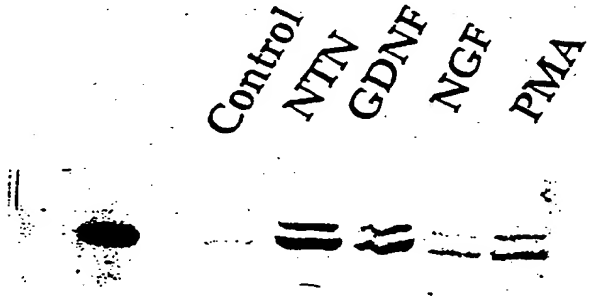
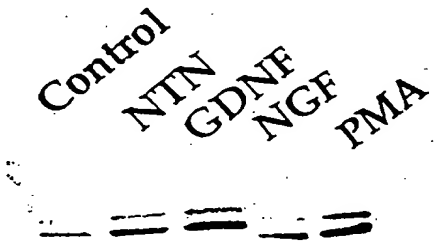


FIGURE 14C SY5Y Neuroblastoma (RX tx)



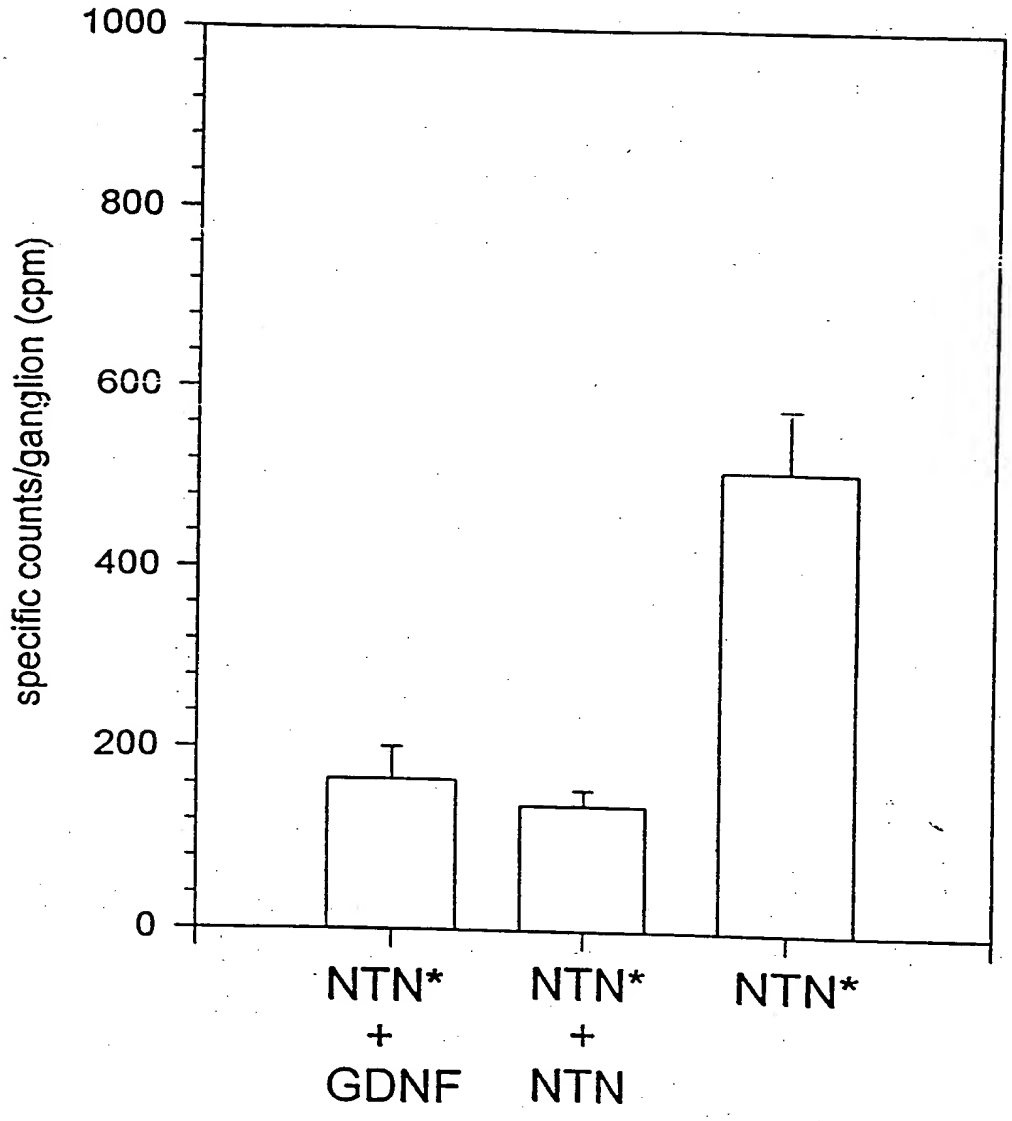

1000
800
600
400
200
0
specific counts/ganglion (cpm)
NTN* + GDNF
NTN* + NTN
NTN*

FIGURE 15

SEQ ID NO:	GROWTH FACTOR	SEQUENCE
134	TGFß1	CCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLDT-------QYSKVLALYNQHNPGASAA-PCCV--PQALEPLPIVYYVGRKPKV--EQLSNMIVRSCKCS
135	TGFß2	CCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSDT-------QHSRVLSLYNTINPEASAS-PCCV--SQDLEPLTILYYIGKTPKI--EQLSNMIVKSCKCS
136	TGFß3	CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSADT-------THSTVLGLYNTLNPEASAS-PCCV--PQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKCS
137	INHßA	CCKKQFFVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAG-TSGSSLSFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYYDDGQNII-KKDIQNMIVEECGCS
138	INHßB	CCRQQFFIDFR-LIGWNDWIIAPTGYYGNYCEGSCPAYLAG-VPGSASSFHTAVVNQYRMRGLNP-GTVNSCCI--PTKLSTMSMLYFDDEYNIV-KRDVPNMIVEECGCA
139	NODAL	CRRVKFQVDFN-LIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPT----NHAYIQSLLKRYQPHR-VPSTCCA--PVKTKPLSMLYVDNGR--VLLEHHKDMIVEECGCL
140	BMP2	CKRHPLYVDFS-DVGWNDWIVAPPGYHAFYCHGECPFPLADHLNST----NHAIVQTLVNSVNS-K-IPKACCV--PTELSAISMLYLDENEKVVLK-NYQDMVVEGCGCR
141	BMP4	CRRHSLYVDFS-DVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYLDEYDKVVLK-NYQEMVVEGCGCR
142	DPP	CRRHSLYVDFS-DVGWDDWIVAPLGYDAYYCHGKCPFPLADHFNST----NHAVVQTLVNNMNPGK-VPKACCV--PTQLDSVAMLYLNDQSTVVLK-NYQEMTVVGCGCR
143	BMP5	CKKHELYVSFR-DLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNAT----NHAIVQTLVHLMFPDH-VPKPCCA--PTKLNAISVLYFDDSSNVILK-KYRNMVVRSCGCH
144	BMP6	CRKHELYVSFQ-DLGWQDWIIAPKGYAANYCDGECSFPLNAHMNAT----NHAIVQTLVHLMNPEY-VPKPCCA--PTKLNAISVLYFDDNSNVILK-KYRNMVVRACGCH
145	BMP7	CKKHELYVSFR-DLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNAT----NHAIVQTLVHFINPET-VPKPCCA--PTQLNAISVLYFDDSSNVILK-KYRNMVVRACGCH
146	BMP8	CRRHELYVSFQ-DLGWLDWVIAPQGYSAYYCEGECSFPLDSCMNAT----NHAILQSLVHLMKPNA-VPKACCA--PTKLSATSVLYYDSSNNVILR-KHRNMVVKACGCH
147	60A	CQMQTLYIDFK-DLGWHDWIIAPEGYGAFYCSGECNFPLNAHMNAT----NHAIVQTLVHLLEPKK-VPKPCCA--PTRLGALPVLYHLNDENVNLK-KYRNMIVKSCGCH
148	BMP3	CARRYLKVDFA-DIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS----NHATIQSIVRAVGVVPGIPEPCCV--PEKMSSLSILFFDENKNVVLKV-YPNMTVESCACR
149	VG1	CKKRHLYVEFK-DVGWQNWVIAPQGYMANYCYGECPYPLTEILNGS----NHAILQTLVHSIEPED-IPLPCCV--PTKMSPISMLFYDNNDNVVLR-HYENMAVDECGCR
150	GDF1	CRARRLYVSFR-EVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPCCV--PARLSPISVLFFDNSDNVVLR-QYEDMVVDECGCR
150	GDF3	CHRHQLFINFQ-DLGWHKWVIAPKGFMANYCHGECPFSMTTYLNSS----NYAFMQALMHMADP-K-VPKAVCV--PTKLSPISMLYQDSDKNVILR-HYEDMVVDECGCG
152	DORSLN	CRRTSLHVNFK-EIGWDSWIIAPKDYEAFECKGGCFFPLTDNVTPT----KHAIVQTLVHLQNPKK-ASKACCV--PTKLDAISILYKDDAGVPTLIYNYEGMKVAECGCR
153	INHα	CHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPVPGAPPTPAQPYSLL-----PGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
154	MIS	CALRELSVDLRAERS----VLIPETYQANNCQGACGWPQSDR----NPRYGNHVVLLLKMQARGATLARPPCCV--PTAYT--GKLLISLSEERISAHHVPNMVATECGCR
155	GDF9	CELHDFSLSFS-QLKWDNWIVAPHSYNPSYCKGDCPSAVSHRYGSPV----HTMVQNMIYE-KLDPSVPSPSCV--PGKYSPLSVLTIEPDGSIAYK-EYEDMMATSCTCR
156	GDNF	CVLTAIHLNVT-DLGLG--YETKEELIFRYCSGSCD-AAETTYDKILKNLSRN------RRLVSDKV-GQACCRPIAFD-DDLSFL-----DDNLVYHILRKHSAKRCGCI
157	NTN	CGLRELEVRVS-ELGLG--YASDETVLFRYÇAGACE-AAARVYDLGLRRLRQR------RRLRRERVRAQPCCRPTAYE-DEVSFL-----DAHSRYHTVHELSARECACV

FIGURE 16

SEQ ID NO:	GROWTH FACTOR	SEQUENCE	
86	TGFß1	CCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLDT-------QYSKVLALYNQHNPGASAA-P	62
87	TGFß2	CCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSDT-------QHSRVLSLYNTINPEASAS-P	62
88	TGFß3	CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSADT-------THSTVLGLYNTLNPEASAS-P	62
89	INHßA	CCKKQFFVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAG-TSGSSLSFHSTVINHYRMRGHSPFANLKS	69
90	INHßB	CCRQQFFIDFR-LIGWNDWIIAPTGYYGNYCEGSCPAYLAG-VPGSASSFHTAVVNQYRMRGLNP-GTVNS	68
91	NODAL	CRRVKFQVDFN-LIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPT----NHAYIQSLLKRYQPHR-VPST	65
92	BMP2	CKRHPLYVDFS-DVGWNDWIVAPPGYHAFYCHGECPFPLADHLNST----NHAIVQTLVNSVNS-K-IPKA	64
93	BMP4	CRRHSLYVDFS-DVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST----NHAIVQTLVNSVNS-S-IPKA	64
94	DPP	CRRHSLYVDFS-DVGWDDWIVAPLGYDAYYCHGKCPFPLADHFNST----NHAVVQTLVNNMNPGK-VPKA	65
95	BMP5	CKKHELYVSFR-DLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNAT----NHAIVQTLVHLMFPDH-VPKP	65
96	BMP6	CRKHELYVSFQ-DLGWQDWIIAPKGYAANYCDGECSFPLNAHMNAT----NHAIVQTLVHLMNPEY-VPKP	65
97	BMP7	CKKHELYVSFR-DLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNAT----NHAIVQTLVHFINPET-VPKP	65
98	BMP8	CRRHELYVSFQ-DLGWLDWVIAPQGYSAYYCEGECSFPLDSCMNAT----NHAILQSLVHLMKPNA-VPKA	65
99	60A	CQMQTLYIDFK-DLGWHDWIIAPEGYGAFYCSGECNFPLNAHMNAT----NHAIVQTLVHLLEPKK-VPKP	65
100	BMP3	CARRYLKVDFA-DIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS----NHATIQSIVRAVGVVPGIPEP	66
101	VG1	CKKRHLYVEFK-DVGWQNWVIAPQGYMANYCYGECPYPLTEILNGS----NHAILQTLVHSIEPED-IPLP	65
102	GDF1	CRARRLYVSFR-EVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLP	69
103	GDF3	CHRHQLFINFQ-DLGWHKWVIAPKGFMANYCHGECPFSMTTYLNSS----NYAFMQALMHMADP-K-VPKA	64
104	DORSLN	CRRTSLHVNFK-EIGWDSWIIAPKDYEAFECKGGCFFPLTDNVTPT----KHAIVQTLVHLQNPKK-ASKA	65
105	INHα	CHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPVPGAPPTPAQPYSLL-----PGAQP	65
106	MIS	CALRELSVDLRAERS----VLIPETYQANNCQGACGWPQSDR----NPRYGNHVVLLLKMQARGATLARPP	63
107	GDF9	CELHDFSLSFS-QLKWDNWIVAPHSYNPSYCKGDCPSAVSHRYGSPV----HTMVQNMIYE-KLDPSVPSP	65
108	GDNF	CVLTAIHLNVT-DLGLG--YETKEELIFRYCSGSCD-AAETTYDKILKNLSRN------RRLVSDKV-GQA	60
109	NTN	CGLRELEVRVS-ELGLG--YASDETVLFRYCAGACE-AAARVYDLGLRRLRQR------RRLRRERVRAQP	61

FIGURE 17

SEQ ID NO:	GROWTH FACTOR	SEQUENCE
110	TGFß1	CCV--PQALEPLPIVYYVGRKPKV--EQLSNMIVRSCKCS
111	TGFß2	CCV--SQDLEPLTILYYIGKTPKI--EQLSNMIVKSCKCS
112	TGFß3	CCV--PQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKCS
113	INHßA	CCV--PTKLRPMSMLYYDDGQNII-KKDIQNMIVEECGCS
114	INHßB	CCI--PTKLSTMSMLYFDDEYNIV-KRDVPNMIVEECGCA
115	NODAL	CCA--PVKTKPLSMLYVDNGR--VLLEHHKDMIVEECGCL
116	BMP2	CCV--PTELSAISMLYLDENEKVVLK-NYQDMVVEGCGCR
117	BMP4	CCV--PTELSAISMLYLDEYDKVVLK-NYQEMVVEGCGCR
118	DPP	CCV--PTQLDSVAMLYLNDQSTVVLK-NYQEMTVVGCGCR
119	BMP5	CCA--PTKLNAISVLYFDDSSNVILK-KYRNMVVRSCGCH
120	BMP6	CCA--PTKLNAISVLYFDDNSNVILK-KYRNMVVRACGCH
121	BMP7	CCA--PTQLNAISVLYFDDSSNVILK-KYRNMVVRACGCH
122	BMP8	CCA--PTKLSATSVLYYDSSNNVILR-KHRNMVVKACGCH
123	60A	CCA--PTRLGALPVLYHLNDENVNLK-KYRNMIVKSCGCH
124	BMP3	CCV--PEKMSSLSILFFDENKNVVLKV-YPNMTVESCACR
125	VG1	CCV--PTKMSPISMLFYDNNDNVVLR-HYENMAVDECGCR
126	GDF1	CCV--PARLSPISVLFFDNSDNVVLR-QYEDMVVDECGCR
127	GDF3	VCV--PTKLSPISMLYQDSDKNVILR-HYEDMVVDECGCG
128	DORSLN	CCV--PTKLDAISILYKDDAGVPTLIYNYEGMKVAECGCR
129	INHα	CCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
130	MIS	CCV--PTAYT--GKLLISLSEERISAHHVPNMVATECGCR
131	GDF9	SCV--PGKYSPLSVLTIEPDGSIAYK-EYEDMMATSCTCR
132	GDNF	CCRPIAFD-DDLSFL-----DDNLVYHILRKHSAKRCGCI
133	NTN	CCRPTAYE-DEVSFL-----DAHSRYHTVHELSARECACV

FIGURE 18